Amendments to the Specification:

Please replace the paragraph beginning at page 13, line 15, with the following redlined paragraph:

--AgfA is characterized as having a two-domain structure with a 22 residue protease-susceptible N-terminal region and a 109 residue protease-resistant C-terminal core region [Collinson, 1999]. This C-terminal core region has five-fold sequence homology as represented in Fig 5B and is predicted to comprise a primarily β–sheet structure. The first 18 amino acids of each of the five segments conformed to the consensus sequence $Sx_5QxGx_2NxAx_3Q$ (SEQ ID NO: 59) separated by 4 or 5 additional residues except for the terminal repeat which ended in Y. Analysis of this five-fold sequence homology has yielded a hypothetical, parallel β–helix, three-dimensional structure for AgfA [Collinson, 1999] and this model is displayed in Figure 5C.--

Please replace the paragraph beginning at page 31, line 13, with the following redlined paragraph:

--The unusually stable and multifunctional, thin aggregative fimbriae common to all *Salmonella* spp. are principally polymers of the fimbrin subunit, AgfA. AgfA of *Salmonella enteritidis* consisted of two domains: a protease-sensitive, 22 amino acid N-terminal region and a protease-resistant, 109 residue C-terminal core. The unusual amino acid sequence of the AgfA core region comprised 2-, 5- and 10-fold internal sequence homology patterns reflected in 5 conserved, 18-residue tandem repeats. These repeats had the consensus sequence, $Sx_5QxGx_2NxAx_3Q$ (SEQ ID NO: 59) and were linked together by 4 or 5 residues, $(x)xAx_2$. The predicted secondary structure for this unusual arrangement of tandem repeats in AgfA indicated mainly extended conformation with the β–strands linked by 4 to 6 residues. Candidate proteins containing motifs of alternating β–strands and short loops were selected from folds described in SCOP as a source of coordinates for AgfA model construction. Three all-β class motifs selected from the *Serratia marcescens* metalloprotease, myelin P2 protein or vitelline membrane outer protein I were used for initial AgfA homology build-up procedures ultimately resulting in three structural models, β barrel, β prism and parallel β helix. The β barrel model suggested a

compact, albeit irregular structure, with the β-strands arranged in two antiparallel β–sheet faces. The β prism model did not reflect the five- or ten-fold symmetry of the AgfA primary sequence. The favored, parallel β helix model was a compact coil of ten helically arranged β–strands forming two parallel β -sheet faces. This arrangement predicted a regular, potentially stable, C-terminal core region consistent with the observed tandem repeat sequences, protease-resistance and strong tendency of this fimbrin to oligomerize and aggregate. Positional conservation of amino acid residues in AgfA and the *E. coli* AgfA homologue, CsgA, provided strong evolutionary support for this model. The parallel β helix model of AgfA offers an interesting solution to a multifunctional fimbrin molecular surface having solvent exposed areas, regions for major and minor subunit interactions as well as fiber-fiber interactions common to many bacterial fimbriae.--

Please replace the paragraph beginning at page 40, line 4, with the following redlined paragraph:

--The five-fold sequence homology within the 109 residue C-terminal core region was extremely regular and consisted of five, tandemly arranged segments (Figure 9c). The first 18 amino acids of each of these five segments conformed to the consensus sequence $Sx_5QxGx_2NxAx_3Q$ (SEQ ID NO: 59) separated by 4 or 5 additional residues except for the terminal repeat which ended in Y (Figure 9c). Homology comparisons between segments C5a:C5d and C5c:C5e were the highest with 50% identity compared to segments C5b:C5d or C5d:C5e with 44% residue identity (Figure 9a,c). The other segment pairs were 39% identical.--

Please replace the paragraph beginning at page 45, line 18, with the following redlined paragraph:

--One feature of the AgfA fimbrin of *Salmonella* thin aggregative fimbriae is the highly conserved, five-fold repeated consensus sequence~~, $SxifixQxGx_2NxAfixQ(x)x_3$~~ comprising 109 residues of the protease resistant C-terminal core region of the fimbrin. This region is preceded by a distinctive, protease-susceptible glycine-rich N-terminus of 17 to 22 residues.

Except for the AgfA fimbrin homologue of *E. coli* curli, CsgA (Hammar *et al.*, 1996), no other fimbrial proteins possess highly conserved, tandem primary amino acid sequence repeat motifs.--